Amendments to the Specification:

- Please replace the paragraph on page 5, line 11 with the following amended paragraph:

Figure 2 – (A) Alignment of the aPP and the GCN4 basic-spacer segment sequences used to guide protein design. Essential DNA-contact residues within GCN4 are in pink; essential folding residues within aPP are in yellow or blue. Conflict positions are indicated by a dashed line. (B) Peptides used and their affinities for hsCRE24. Equilibrium dissociation constants of stable $PPBR^{SR}$-hsCRE complexes are listed at right. All peptides except G_{56} and G_{27} contained GGC sequences at their carboxyl termini. G_{27} contained a single cysteine. The carboxy-terminal cysteine was alkylated with bromoacetamide to study protein monomers ($PPBR^{SR}$ & G_{27}) or oxidized to study disulfide-linked dimers ($PPBR^{SS}$). SEQ ID NOs: 6-14 are shown.

- Please replace the paragraph on page 5, line 20 with the following amended paragraph:

Figure 3 – (A) Residues of PPBR4 targeted for variation mapped onto the crystal structure of aPP. Side chains varied in library A are in yellow, those varied in library B are in green. (B) Sequences of PPBR4 and the two libraries. Residues varied are indicated by an X. Each position was randomized at the DNA level using the NNS codon scheme. (C) Sequences of the N-terminal amino acids deduced from the DNA sequences of the library B clones after three selection rounds. Peptides containing the boxed sequences followed by the remaining residues of PPBR4 were synthesized and their properties investigated *in vitro*. SEQ ID NOs: 15-22 are shown.

- Please replace the paragraph on page 5, line 28 with the following amended paragraph:

Figure 4 – Seven distinct sequences isolated from BAKLIB phage library. Dissociation constants for miniature protein binding to Bcl-2 are shown on the right. SEQ ID NOs: 22-30 are shown.

- Please replace the paragraph on page 5, line 30 with the following amended paragraph:

Figure 5 – Sequences of the p53 miniature proteins which inhibit p53 binding to hDM2. Residues that stabilize the aPP core are in yellow or blue, residues that contribute to binding hDM2 are in purple, residues identified by phage display are in red. Equilibrium dissociation constants of stable $PPBR^{SR}$-hsCRE complexes are listed at right. SEQ ID NOs: 31-37 are shown. The aPP sequence comprises residues 1-31 of SEQ ID NO: 6.

- Please replace the paragraph on page 6, line 3 with the following amended paragraph:

Figure 6 – Two views of the universal library that illustrate the relative orientation of the six residues chosen for variation (in beige) on the aPP solvent-exposed face (top). The image on the left sites along the alpha helix axis; the image on the right sites perpendicular to the alpha helix axis. Residues in blue contribute to forming the aPP hydrophobic core. Alignment of aPP and the universal library (bottom). Residues in blue stabilize the aPP hydrophobic core; residues in red are targeted for variation. SEQ ID NO: 38 is shown. The aPP sequence comprises residues 1-31 of SEQ ID NO: 6.